

- C¹
- c) a biologically-active fragment of the amino acid sequence of SEQ ID NO:1, and
 - d) an antigenically-active fragment of the amino acid sequence of SEQ ID NO:1.

C²

18. (Once Amended.) The method of claim [17] 20, wherein before hybridization, the [nucleic acid material of the biological sample] target polynucleotide is amplified by the polymerase chain reaction.

Please add the following new claims:

- Sub D1
19. An isolated polynucleotide selected from the group consisting of:
- a) a polynucleotide sequence of SEQ ID NO:2,
 - b) a naturally-occurring polynucleotide sequence having at least 90% sequence identity to the sequence of SEQ ID NO:2 and
 - b) a polynucleotide sequence complementary to a) or b).
- C³
20. A method of detecting a target polynucleotide in a sample, said target polynucleotide having the sequence of a polynucleotide of claim 19, comprising
- hybridizing the sample with a probe comprising at least 16 contiguous nucleotides comprising a sequence complementary to said target polynucleotide in the sample, and which probe specifically hybridizes to said target polynucleotide, under conditions whereby a hybridization complex is formed between said probe and said target polynucleotide, and
 - detecting the presence or absence of said hybridization complex, and, optionally, if present, the amount thereof.
- Sub G3
21. A method of claim 20, wherein the probe comprises at least 30 contiguous nucleotides.
22. A method of claim 20, wherein the probe comprises at least 60 contiguous nucleotides.